AMENDMENTS TO THE SPECIFICATION

Please replace paragraph [0043] in the application as filed with the following amended paragraph:

[0043] ~~Chain imbalances~~ A linkage disequilibrium between SNPs that can be analyzed are thought to occur when the physical distance between SNP positions is about 10,000 to 100,000 nucleotide bases. Therefore, when [[the]] approximately 100,000 SNPs contained in the first `scanning domain` cover the entire length of the ~~approximately 100,000~~ chromosomes, it is preferred that the first typing be performed for about 1,000 SNPs.

Please replace paragraph [0076] in the application as filed with the following amended paragraph:

[0076] However, as described above, it is very difficult to select and directly type a `target` SNP. This problem is solved by applying the ~~chain imbalance~~ linkage disequilibrium between the `target` SNP and the nearby SNPs, and by estimating the domain near the `target` SNP. The nearby SNP with the ~~chain imbalance~~ linkage disequilibrium is weak when compared with when the `target` SNP is analyzed directly, and similarly, it is expected that the probability distribution of the haplotype will change. This kind of nearby SNP is considered to be a `marker` SNP for the `target` SNP. In other words, the statistical amount of the sample that is the object of analysis (group with effect: Case group) is compared with the reference statistical amount of the reference sample (group having no effect: Control group) and when the difference exceeds a preset threshold value, it is determined that there was change in the corresponding typing domain (estimated as the marker SNP), and a specified ratio (for example 1/5 to 1/10) with respect to that typing domain is set as a new scanning domain, and the next processing cycle is performed.